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## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Currently only blastn and blastp programs are available. Using sequences > 150 Kb is not recommended.

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties  
gap x\_dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI

Light Chain CDR1

or sequence in FASTA format from:  to:

KTSQDINKYMA

Marine 21.6

Sequence 2 Enter accession or GI

or sequence in FASTA format from:  to:

RSSQSLAKSYGNTYLS

residues 44-59 of  
SEQ ID NO:12

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

Credits to: Tatiana Tatusov and Tom Madden

EXHIBIT

A

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]**

Matrix  BLOSUM62  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

Sequence 1 lcl|seq\_1 Length 11

Sequence 2 lcl|seq\_2 Length 16

No significant similarity was found

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Program  blastp  Matrix 0 BLOSUM62

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties  
gap x dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI  or sequence in FASTA format from:  to:

Heavy chain CDR3

EGYYGNYGVYAMDY

Marine 21.6

Sequence 2 Enter accession or GI

or sequence in FASTA format from:  to:

GGYDGWDYADY

residues 118 - 129 of  
SEQ ID NO: 15

Comments and suggestions to: [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)

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EXHIBIT

F

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Help](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]**

Matrix  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

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Sequence 1 lcl|seq\_1 Length 14

Sequence 2 lcl|seq\_2 Length 12

No significant similarity was found

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Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Open gap  and extension gap  penalties  
gap x dropoff  expect  word size  Filter

Sequence 1 Enter accession or GI

Light Chain CDR3

or sequence in FASTA format from:  to:

LQYDNLWT

mouse 21.6

Sequence 2 Enter accession or GI

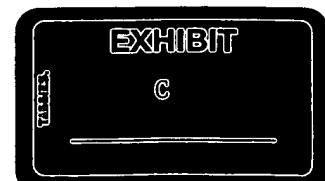
or sequence in FASTA format from:  to:

LQGTHQPYT

Residues 114-122 of  
SEQ ID NO: 12

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Matrix  BLOSUM62  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter  Align

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**Sequence 1 lcl|seq\_1 Length 8****Sequence 2 lcl|seq\_2 Length 9**

No significant similarity was found